

EXHIBIT A:
MOUSE LKB1 COMPARED TO HUMAN LKB1

BLAST**Basic Local Alignment Search Tool**[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

SEQ ID NO: 6 (44-343) Compared to Mouse LKB1Results for: lcl|41549 SEQ ID NO: 6(433aa)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID lcl|41549 lcl|41549**Description**

SEQ ID NO: 6

Molecule type

amino acid

Query Length

433

Subject ID

gi|7106425|ref|NP_035622.1|

Description

serine/threonine-protein kinase 11 [Mus musculus] >gi|81917862|sp|Q9WTK7.1|STK11_MOUSE RecName: Full=Serine/threonine-protein kinase 11; AltName: Full=Serine/threonine-protein kinase LKB1 >gi|4838565|gb|AAD31044.1|AF145287_1 Peutz-Jeghers syndrome kinase LKB1 [Mus musculus] >gi|6649101|gb|AAF21370.1|AF151711_1 protein kinase LKB1 [Mus musculus] >gi|4530575|gb|AAD22100.1|serine/threonine-protein kinase LKB1 [Mus musculus] >gi|4589404|dbj|BAA76749.1|LKB1 [Mus musculus] >gi|5901683|gb|AAD55368.1|Peutz-Jeghers syndrome protein [Mus musculus] >gi|30851173|gb|AAH52379.1| Serine/threonine kinase 11 [Mus musculus] >gi|74186437|dbj|BAE42977.1| unnamed protein product [Mus musculus] >gi|74192527|dbj|BAE43050.1| unnamed protein product [Mus musculus] >gi|117616790|gb|ABK42413.1| Stk11 [synthetic construct] >gi|148699653|gb|EDL31600.1| serine/threonine kinase 11, isoform CRA_a [Mus musculus]

Molecule type

amino acid

Subject Length

436

ProgramBLASTP 2.2.24+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) | [Taxonomy reports](#) | [Multiple alignment](#)[Search Parameters](#)**Search parameter name** **Search parameter value**

Program	blastp
Query range	44-343
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Low Complexity Filter	Yes
Filter string	L;
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Karlin-Altschul statistics

Params Ungapped Gapped

Lambda	0.320459	0.267
K	0.139595	0.041
H	0.429592	0.14

[Results Statistics](#)**Results Statistics parameter name** **Results Statistics parameter value**

Effective search space	110297
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Graphic Summary

Distribution of Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

Dot Matrix View**Plot of Icl|41549 vs gi|7106425|ref|NP_035622.1| [?]**

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

**Descriptions**

Sequences producing significant alignments:	Score (Bits)	E Value
<u>ref NP_035622.1 serine/threonine-protein kinase 11 [Mus musculus]</u>	526	4e-154

Alignments

>ref|NP_035622.1| serine/threonine-protein kinase 11 [Mus musculus]
 sp|Q9WTK7.1|STK11_MOUSE RecName: Full=Serine/threonine-protein kinase 11; AltName: Full=Serine/threonine-protein kinase LKB1
 gb|AAD31044.1|AF145287_1 Peutz-Jeghers syndrome kinase LKB1 [Mus musculus]
 9 more sequence titles

gb|AAF21370.1|AF151711_1 protein kinase LKB1 [Mus musculus]
 gb|AAD22100.1| serine/threonine-protein kinase LKB1 [Mus musculus]
 dbj|BAA76749.1| LKB1 [Mus musculus]
 gb|AAD55368.1| Peutz-Jeghers syndrome protein [Mus musculus]
 gb|AAH52379.1| Serine/threonine kinase 11 [Mus musculus]
 dbj|BAB42977.1| unnamed protein product [Mus musculus]
 dbj|BAB43050.1| unnamed protein product [Mus musculus]
 gb|ABK42413.1| Stk11 [synthetic construct]
 gb|EDL31600.1| serine/threonine kinase 11, isoform CRA_a [Mus musculus]

Length=436

Score = 526 bits (1354), Expect = 4e-154, Method: Compositional matrix adjust.
 Identities = 288/300 (96%), Positives = 292/300 (98%), Gaps = 0/300 (0%)

Query 44	KLIGKYLMGDLLEGGSYGKVKEVILDSETLCRRRAVKKLRLRRIIPNGEANVKKERIQLLR	103
Sbjct 44	KLIGKYLMGDLLEGGSYGKVKEVILDSETLCRRRAVKKLRLRRIIPNGEANVKKERIQLLR	103
Query 104	RLLRKHNVVIQLVDVLYNEEKQKMMVMMEYCVCGMQUEMLDSVEEKRFPVQCQAHGYFCQLIDG	163
	RLLRH+NVIQLVDVLYNEEKQKMMVMMEYCVCGMQUEMLDSVEEKRFPVQCQAHGYF QLIDG	
Sbjct 104	RLLRKHNVVIQLVDVLYNEEKQKMMVMMEYCVCGMQUEMLDSVEEKRFPVQCQAHGYFQLIDG	163
Query 164	LEYLHSQGIVHKDKIPgnllltttgtt1KISDLGVFAEALHPFAADDTCRTSQGSPAFQPPE	223
	LEYLHSQGIVHKDKIPgnllltttgtt1GTLKISDLGVFAEALHPFA DDTCRTSQGSPAFQPPE	
Sbjct 164	LEYLHSQGIVHKDKIPGNLTTNGTLKISDLGVFAEALHPFAVDDTCRTSQGSPAFQPPE	223
Query 224	IANGLDTFSGFKVDIWSAGVTLYNITTGLYPFEGDNITYKLFEENIGKGSYAIPGDCGPPLS	283
	IANGLDTFSGFKVDIWSAGVTLYNITTGLYPFEGDNITYKLFEENIG+G + IP DCGPPLS	
Sbjct 224	IANGLDTFSGFKVDIWSAGVTLYNITTGLYPFEGDNITYKLFEENIGRGDFTIPDCGPPLS	283
Query 284	DLLKGMLYEPAKRPISIQTIRQHNSWFRKKHppaeapvpippspDTKDRNRMSMTVVVPYLED	343
	DLL+GMLEYEPAKRPISIQTIRQHNSWFRKKH AEA VPIPSPDPTKDRNRMSMTVVVPYLED	
Sbjct 284	DLLRGMLYEPAKRPISIQTIRQHNSWFRKKHPLAEALVPIPSPDPTKDRNRMSMTVVVPYLED	343